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## SEQUENCE LISTING

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<120> GLYCOSYLTRANSFERASES OF HELICOBACTER PYLORI AS A NEW TARGET IN PREVENTION AND TREATMENT OF H. PYLORI INFECTIONS

<130> 12243.24USWO

<140> 10/019,214

<141> 2001-12-21

<150> PCT/CA00/00777

<151> 2000-06-28

<150> 60/140,820

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<170> PatentIn Ver. 2.1

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Glu Gly Gly Leu His Pro Leu Val Lys Lys His Leu His Pro Tyr Phe 50 55 60

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Glu Val Ser Lys Phe Tyr Tyr Ala Leu Lys Tyr His Ala Lys Phe Met 85 90 95

Ser Leu Gly Glu Leu Gly Cys Tyr Ala Ser His Tyr Ser Leu Trp Glu 100 105 110

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Arg Val Gly Ile Ile Lys Ala Tyr Ser Glu Gly Val Gly Thr Gln Gly 180 185 190

Tyr Val Ile Thr Pro Lys Ile Ala Lys Val Phe Leu Lys Cys Ser Arg 195 200 205

Lys Trp Val Val Pro Val Asp Thr Ile Met Asp Ala Thr Phe Ile His 210 215 220

Gly Val Lys Asn Leu Val Leu Gln Pro Phe Val Ile Ala Asp Asp Glu 225 230 235 240

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Tyr Pro Glu Gln Asp Leu Leu Thr Leu Ala Cys Tyr Gln Lys Val Leu
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gtttatcaaa accgccagga gttgttttct caaatttatg ggcatgtttt tgataacccc 420
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Gly Phe Ala Gln Phe Phe Arg Ser Leu Phe Leu Ser His Ala Ile Ala 115 120 Pro Ala Pro Lys Glu Tyr His Gln Val Glu Lys Tyr Cys Phe Leu Phe 135 Ser Gln Phe Leu Glu Lys Glu Leu Asp Gln Lys Ser Val Leu Pro Leu Lys Leu Ala Phe Asn Leu Pro Thr His Thr Pro Asn Thr Pro Lys Lys 170 Ile Gly Phe Asn Pro Ser Ala Ser Tyr Gly Ser Ala Lys Arg Trp Pro Ala Ser Tyr Tyr Ala Glu Val Ser Ala Val Leu Leu Glu Lys Gly His 200 Glu Ile Tyr Phe Phe Gly Ala Lys Glu Asp Ala Ile Val Ser Glu Glu 210 215 Ile Leu Lys Leu Ile Lys Gly Ser Leu Lys Asn Pro Ser Leu Phe His 230 235 Asn Ala Tyr Asn Leu Cys Gly Lys Thr Ser Ile Glu Glu Leu Ile Glu 250 Arg Ile Ala Val Leu Asp Leu Phe Ile Thr Asn Asp Ser Gly Pro Met His Val Ala Ala Ser Met Gln Thr Pro Leu Ile Ala Leu Fhe Gly Pro Thr Asp Glu Lys Glu Thr Arg Pro Tyr Lys Ala Gln Lys Thr Ile Val Leu Asn His His Leu Ser Cys Ala Pro Cys Lys Lys Arg Val Cys Pro 305 315 Leu Lys Asn Ala Lys Asn His Leu Cys Met Lys Ser Ile Thr Pro Leu 330 Glu Val Leu Glu Ala Ala His Thr Leu Leu Glu Glu Pro 345 <210> 9 <211> 822 <212> DNA <213> Helicobacter pylori <400> 9 ttgcgtattt ttatcatttc tttaaatcaa aaagtgtgcg ataaatttgg tttggttttt 60 agagacacca cgactttact caatagcatc aatgccaccc accaccaagt gcaaattttt 120 gatgcgattt attctaaaac ttttgaaggc gggttgcacc ccttagtgaa aaagcattta 180 cacccttatt tcatcacgca aaacatcaaa gacatgggaa ttacaaccag tctcatcagt 240 gaggtttcta agttttatta cgctttaaaa taccatgcga agtttatgag cttgggagag 300 cttgggtgct atgcgagcca ttattccttg tgggaaaaat gcatagaact caatgaagcg 360 atctgtattt tagaagacga tataaccttg aaagaggatt ttaaagaggg cttqqatttt 420 ttagaaaaac acatccaaga gttaggctat gttcgcttga tgcatttatt atatgatccc 480 aatattaaaa gtgagccatt gaaccataaa aaccacgaga tacaagagcg tgtagggatt 540 attaaagctt atagcgaagg ggtggggact caaggctatg tgatcacgcc caagattgcc 600 aaagttttta aaaaacacag ccgaaaatgg gttgttcctg tggatacgat aatggacgct 660 acttttatcc atggcgtgaa aaatctggtg ttacaacctt ttgtgatcgc tgatgatgag 720 caaatctcta cgatagcgcg aaaagaacaa ccttatagcc ctaaaaatcgc cttaatgaga 780 gaactccatt ttaaatattt gaaatattgg cagtttatat ag 822

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Glu Gly Gly Leu His Pro Leu Val Lys Lys His Leu His Pro Tyr Phe 50 55 60

Ile Thr Gln Asn Ile Lys Asp Met Gly Ile Thr Thr Ser Leu Ile Ser
65 70 75 80

Glu Val Ser Lys Phe Tyr Tyr Ala Leu Lys Tyr His Ala Lys Phe Met 85 90 95

Ser Leu Gly Glu Leu Gly Cys Tyr Ala Ser His Tyr Ser Leu Trp Glu 100 105 110

Lys Cys Ile Glu Leu Asn Glu Ala Ile Cys Ile Leu Glu Asp Asp Ile 115 120 125

Thr Leu Lys Glu Asp Phe Lys Glu Gly Leu Asp Phe Leu Glu Lys His 130 135 140

Ile Gln Glu Leu Gly Tyr Val Arg Leu Met His Leu Leu Tyr Asp Pro 145 150 155 160

Asn Ile Lys Ser Glu Pro Leu Asn His Lys Asn His Glu Ile Gln Glu
165 170 175

Arg Val Gly Ile Ile Lys Ala Tyr Ser Glu Gly Val Gly Thr Gln Gly 180 185 190

Tyr Val Ile Thr Pro Lys Ile Ala Lys Val Phe Lys Lys His Ser Arg 195 200 205

Lys Trp Val Val Pro Val Asp Thr Ile Met Asp Ala Thr Phe Ile His 210 215 220

Gly Val Lys Asn Leu Val Leu Gln Pro Phe Val Ile Ala Asp Asp Glu 225 230 235 240 Gln Ile Ser Thr Ile Ala Arg Lys Glu Gln Pro Tyr Ser Pro Lys Ile 245 250 255

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Glu His Pro Gln Ser Gln Asn Asp Ser Glu Lys Leu Phe Tyr Lys Ile
35 40

His Cys Leu Val Asp Asn Leu Ser Leu Glu Asn Gln Cys Lys Leu Lys 50 60

Glu Thr Leu Ala Pro Phe Ser Ala Phe Met Ser Val Asp Phe Leu Asp 65 70 75 80

Ile Ser Thr Pro Asn Leu Tyr Thr Pro Ser Ile Glu Pro Ser Ala Ile 85 90 95 Asp Lys Ile Asn Glu Ala Phe Leu Gln Leu Asn Ile Tyr Ala Lys Thr 100 105 110

Arg Phe Ser Lys Met Val Met Cys Arg Leu Phe Leu Ala Ser Leu Phe 115 120 125

Pro Gln Tyr Asp Lys Ile Ile Met Phe Asp Ala Asp Thr Leu Phe Leu 130 135 140

Asn Asp Val Ser Glu Ser Phe Phe Ile Pro Leu Asp Gly Tyr Tyr Phe 145 150 155 160

Gly Ala Ala Lys Asp Phe Ser Ser Pro Lys Asn Leu Lys His Phe Gln 165 170 175

Thr Glu Arg Glu Arg Glu Pro Arg Gln Lys Phe Phe Leu His Glu His 180 185 190

Tyr Leu Lys Glu Lys Asp Met Lys Ile Ile Cys Glu Asn His Tyr Asn 195 200 205

Val Gly Phe Leu Ile Val Asn Leu Lys Leu Trp Arg Ala Asp His Leu 210 215 220

Glu Glu Arg Leu Leu Asn Leu Thr His Gln Lys Gly Gln Cys Val Phe 225 230 235 240

Cys Pro Glu Gln Asp Ile Leu Thr Leu Ala Cys Tyr Gln Lys Val Leu 245 250 255

Gln Leu Pro Tyr Ile Tyr Asn Thr His Pro Phe Met Val Asn Gln Lys 260 265 270

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Val Gly Lys Pro Trp Val Leu Pro Thr Ala Leu Tyr Ser Lys Glu Trp 290 295 300

His Glu Thr Leu Leu Lys Thr Pro Phe Tyr Ala Glu Tyr Ser Val Lys 305 310 315 320

Phe Leu Lys Gln Met Thr Glu Phe Leu Ser Leu Lys Asp Lys Gln Lys 325 330 335

Thr Phe Glu Phe Leu Ala Pro Leu Leu Asn Lys Lys Thr Leu Leu Glu 340 345 350

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Lys His Phe Glu Ile Ile Pro Val Phe Lys Asn Ile Pro Ala Phe Tyr
Asp Leu Lys Lys Gln Gly Val Phe Trp Ala Met Lys Asp Phe Leu Trp
Leu Leu Lys Ala Leu Lys Lys His Lys Ile Lys His Leu Ile Leu Glu
Lys Gln Asp Phe Arg Ser Ala Leu Leu Ser Lys Phe Val Ser Ile Thr
Thr Pro Asn Lys Glu Ile Lys Asn Ala Tyr Gln Asn Arg Gln Glu Leu
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Asn Asn Arg Asn Ile Ser Leu Glu His Leu Gln Ile Val Leu Lys Leu
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25

20

Lys His Phe Glu Ile Ile Pro Ile Phe Glu Asn Ile Pro Ala Phe Tyr 50 55 60

Asp Leu Lys Lys Gln Gly Val Phe Trp Ala Met Lys Asp Phe Leu Trp Leu Leu Lys Ala Ile Lys Lys His Lys Ile Lys His Leu Ile Leu Glu Lys Gln Asp Phe Arg Ser Phe Leu Leu Ser Lys Phe Val Ser Ile Thr 105 Thr Pro Asn Lys Glu Ile Lys Asn Val Tyr Gln Asn Arg Gln Glu Leu Phe Ser Pro Ile Tyr Gly His Val Phe Asp Asn Pro Pro Tyr Pro Met 135 Asn Leu Lys Asn Pro Lys Lys Ile Leu Ile Asn Pro Phe Thr Arg Ser Ile Glu Arg Ser Ile Pro Leu Glu His Leu Lys Ile Val Leu Lys Leu 165 170 Leu Lys Pro Phe Cys Val Thr Leu Leu Asp Phe Glu Glu Arg Tyr Ala Phe Leu Gln Asn Glu Ala Thr His Tyr Arg Ala Lys Thr Ser Leu Glu Glu Val Lys Ser Leu Ile Leu Glu Ser Asp Leu Tyr Ile Gly Gly Asp Ser Phe Leu Ile His Leu Ala Tyr Tyr Leu Lys Lys Asn Tyr Phe Ile Phe Phe Tyr Arg Asp Asn Asp Asp Phe Met Pro Pro Asn Gly Lys Lys 245 250 255 Glu Asn Phe Leu Lys Ala His Lys Ser His Tyr Ile Glu Gln Asp Leu

265

Ala Lys Lys Phe Arg His Leu Gly Leu Ile Ile

280

275